

SEQUENCE LISTING

<110> Nielsen, Bjarne R.
Nielsen, Ruby
Lehmbeck, Jan

<120> Thermostable Glucoamylase

<130> 5279.210-US

<160> 35

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Talaromyces emersonii

<220>

<221> misc_feature

<222> (13)..(13)

<223> Xaa at position 13 denotes an undetermined amino acid

<400> 1

Ala	Asn	Gly	Ser	Leu	Asp	Ser	Phe	Leu	Ala	Thr	Glu	Xaa	Pro	Ile	Ala
1				5				10						15	

Leu	Gln	Gly	Val	Leu	Asn	Asn	Ile	Gly
			20				25	

<210> 2

<211> 20

<212> PRT

<213> Talaromyces emersonii

<400> 2

Val	Gln	Thr	Ile	Ser	Asn	Pro	Ser	Gly	Asp	Leu	Ser	Thr	Gly	Gly	Leu
1				5				10						15	

Gly	Glu	Pro	Lys
			20

<210> 3

<211> 22

<212> PRT

<213> Talaromyces emersonii

<220>

<221> misc_feature

<222> (1)..(1)
 <223> Xaa in positions 1 denotes an undetermined amino acid

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> Xaa in positions 12 denotes an undetermined amino acid

<400> 3

Xaa Asn Val Asn Glu Thr Ala Phe Thr Gly Pro Xaa Gly Arg Pro Gln
 1 5 10 15

Arg Asp Gly Pro Ala Leu
 20

<210> 4
 <211> 35
 <212> PRT
 <213> Talaromyces emersonii

<400> 4

Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly
 1 5 10 15

Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala
 20 25 30

Asn His Lys
 35

<210> 5
 <211> 16
 <212> PRT
 <213> Talaromyces emersonii

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> Xaa in position 2 denotes an undetermined amino acid

<400> 5

Thr Xaa Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys
 1 5 10 15

<210> 6

<211> 35
 <212> PRT
 <213> Talaromyces emersonii

<400> 6

Ala Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
 1 5 10 15

Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu Asp Asp
 20 25 30 .

Ser Trp Gln
 35

<210> 7
 <211> 591
 <212> PRT
 <213> Talaromyces emersonii

<400> 7

Ala Thr Gly Ser Leu Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala
 1 5 10 15

Leu Gln Gly Val Leu Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala
 20 25 30

Gly Ala Ser Ala Gly Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro
 35 40 45

Asn Tyr Phe Tyr Ser Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr
 50 55 60

Leu Val Asp Ala Phe Asn Arg Gly Asn Lys Asp Leu Glu Gln Thr Ile
 65 70 75 80

Gln Gln Tyr Ile Ser Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro
 85 90 95

Ser Gly Asp Leu Ser Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn Val
 100 105 110

Asn Glu Thr Ala Phe Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly
 115 120 125

Pro Ala Leu Arg Ala Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile
 130 135 140

Asp Asn Gly Glu Ala Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val
 145 150 155 160

Gln Asn Asp Leu Ser Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe
 165 170 175

Asp Leu Trp Glu Glu Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val
 180 185 190

Gln His Arg Ala Leu Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn
 195 200 205

His Thr Cys Ser Asn Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe
 210 215 220

Leu Gln Ser Tyr Trp Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly
 225 230 235 240

Ser Gly Arg Ser Gly Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His
 245 250 255

Thr Phe Asp Pro Ala Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys
 260 265 270

Ser Ala Arg Ala Leu Ala Asn His Lys Val Val Thr Asp Ser Phe Arg
 275 280 285

Ser Ile Tyr Ala Ile Asn Ser Gly Ile Ala Glu Gly Ser Ala Val Ala
 290 295 300

Val Gly Arg Tyr Pro Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr
 305 310 315 320

Leu Ala Thr Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln
 325 330 335

Trp Lys Lys Ile Gly Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe
 340 345 350

Phe Gln Asp Ile Tyr Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly

355	360	365
Ser Thr Thr Phe Asn Asp 370	Ile Ile Ser Ala Val 375	Gln Thr Tyr Gly Asp 380
Gly Tyr Leu Ser Ile Val 385	Glu Lys Tyr Thr Pro 390	Ser Asp Gly Ser Leu 395
Thr Glu Gln Phe Ser Arg 405	Thr Asp Gly Thr Pro 410	Leu Ser Ala Ser Ala 415
Leu Thr Trp Ser Tyr Ala 420	Ser Leu Leu Thr Ala 425	Ser Ala Arg Arg Gln 430
Ser Val Val Pro Ala Ser 435	Trp Gly Glu Ser Ser 440	Ala Ser Ser Val Leu 445
Ala Val Cys Ser Ala Thr 450	Ser Ala Thr Gly Pro 455	Tyr Ser Thr Ala Thr 460
Asn Thr Val Trp Pro Ser 465	Ser Ser Gly Ser Gly 470	Ser Ser Thr Thr Thr 475
Ser Ala Pro Cys Thr Thr 485	Pro Thr Ser Val Ala 490	Val Thr Phe Asp Glu 495
Ile Val Ser Thr Ser Tyr 500	Gly Glu Thr Ile Tyr 505	Leu Ala Gly Ser Ile 510
Pro Glu Leu Gly Asn Trp 515	Ser Thr Ala Ser Ala 520	Ile Pro Leu Arg Ala 525
Asp Ala Tyr Thr Asn Ser 530	Asn Pro Leu Trp Tyr 535	Val Thr Val Asn Leu 540
Pro Pro Gly Thr Ser Phe 545	Glu Tyr Lys Phe Phe 550	Lys Asn Gln Thr Asp 555
Gly Thr Ile Val Trp Glu 565	Asp Asp Pro Asn Arg 570	Ser Tyr Thr Val Pro 575
Ala Tyr Cys Gly Gln Thr 580	Thr Ala Ile Leu Asp 585	Asp Ser Trp Gln 590

<210> 8
 <211> 1605
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(1602)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(72)
 <223>

<220>
 <221> mat_peptide
 <222> (73)..()
 <223>

<400> 8
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 Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 -20 -15 -10
 ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc 96
 Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
 -5 -1 1 5
 aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg 144
 Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
 10 15 20
 gac ggt gct tgg gtg tcg ggc gcg gac tct ggc att gtc gtt gct agt 192
 Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 25 30 35 40
 ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct 240
 Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 45 50 55
 ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc 288
 Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 60 65 70
 agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc 336
 Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 75 80 85
 cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc 384
 Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 90 95 100

ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp 105 110 115 120	432
gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile 125 130 135	480
ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr 140 145 150	528
gac att gtt tgg ccc ctc gtt agg aac gac ctg tcg tat gtg gct caa Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln 155 160 165	576
tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tcg Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser 170 175 180	624
tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser 185 190 195 200	672
gcc ttc gcg acg gcc gtc ggc tcg tcc tgc tcc tgg tgt gat tct cag Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln 205 210 215	720
gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe 220 225 230	768
att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr 235 240 245	816
ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp 250 255 260	864
tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu 265 270 275 280	912
gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser 285 290 295	960
gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr 300 305 310	1008
aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu 315 320 325	1056

tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca	1104
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr	
330 335 340	
gat gtg tcg ctg gac ttc ttc aag gca ctg tac agc gat gct gct act	1152
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr	
345 350 355 360	
ggc acc tac tct tcg tcc agt tcg act tat agt agc att gta gat gcc	1200
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala	
365 370 375	
gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc	1248
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala	
380 385 390	
gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag	1296
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu	
395 400 405	
cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc	1344
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr	
410 415 420	
gcc aac aac cgt cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc	1392
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr	
425 430 435 440	
tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt	1440
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly	
445 450 455	
acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act	1488
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr	
460 465 470	
ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc	1536
Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr	
475 480 485	
tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc	1584
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr	
490 495 500	
cgc tct ggt atg tca ctg tga	1605
Arg Ser Gly Met Ser Leu	
505 510	

<210> 9
 <211> 534
 <212> PRT
 <213> *Aspergillus niger*

<400> 9

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly

-20	-15	-10
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser		
-5	-1 1	5
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala		
10	15	20
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser		
25	30	35 40
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser		
45	50	55
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr		
60	65	70
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val		
75	80	85
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu		
90	95	100
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp		
105	110	115 120
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile		
125	130	135
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr		
140	145	150
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln		
155	160	165
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser		
170	175	180
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser		
185	190	195 200
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln		
205	210	215

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
 220 225 230

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
 235 240 245

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
 250 255 260

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
 265 270 275 280

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
 285 290 295

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
 300 305 310

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
 315 320 325

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
 330 335 340

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
 345 350 355 360

Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
 365 370 375

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
 380 385 390

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
 395 400 405

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
 410 415 420

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
 425 430 435 440

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
445 450 455

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
460 465 470

Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
475 480 485

Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
490 495 500

Arg Ser Gly Met Ser Leu
505 510

<210> 10
<211> 534
<212> PRT
<213> Aspergillus niger

<220>
<221> SIGNAL
<222> (1) .. (24)
<223>

<400> 10

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
1 5 10 15

Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
20 25 30

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
35 40 45

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
50 55 60

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65 70 75 80

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
85 90 95

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 100 105 110

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 115 120 125

Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
 130 135 140

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
 145 150 155 160

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
 165 170 175

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
 180 185 190

Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
 195 200 205

Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
 210 215 220

Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
 225 230 235 240

Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
 245 250 255

Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
 260 265 270

Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
 275 280 285

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
 290 295 300

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
 305 310 315 320

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
325 330 335

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
340 345 350

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
355 360 365

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
370 375 380

Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385 390 395 400

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
405 410 415

Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
420 425 430

Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
435 440 445

Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
450 455 460

Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465 470 475 480

Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
485 490 495

Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
500 505 510

Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
515 520 525

Arg Ser Gly Met Ser Leu
530

<210> 11

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> n in position 3 = A, G, C, T

<400> 11
gtntttraaya ayathgg

17

<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> n= A, G, C, T

<220>
<221> misc_feature
<222> (6)..(6)
<223> n= A, G, C, T

<400> 12
gtnctnaaya ayathgg

17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (6)..(6)
<223> N= A, G, C, T

<400> 13
ctr ganaccc tyctyca

17

<210> 14
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 14
 ctraayaccc tyctyca

17

<210> 15
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> N= A, G, C, T

<400> 15
 accctyctrc trggntt

17

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 16
 gtgagcccaa gttcaatgtg

20

<210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 17
 agaaatcggg tatcctttca g

21

<210> 18

<211> 105
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 18
 gctcctcatg gtggatcccc agttgtgtat atagaggatt gaggaaggaa gagaagtgtg 60
 gatagaggta aattgagttg gaaactccaa gcatggcatc cttgc 105

 <210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 19
 gacagatctc caccatggcg tccctcgttg 30

 <210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 20
 gacctcgagt cactgccaac tatcgtc 27

 <210> 21
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 21
 ccctcaccag gggaatgctg cagttgatg 29

 <210> 22
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 22
cgccattctc ggcgactt 18

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cgccgcggta ttctgcag 18

<210> 24
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
caatataaac gacggtaccc gggagatctc caccatggcg tccctcgttg 50

<210> 25
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
ctaattacat catgcggccc tctagatcac tgccaactat cgtc 44

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
aatttgggtc gctcctgctc g 21

<210> 27
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer

 <400> 27
 cgagcaggag cgacccaaat tatttctact cctggacacg 40

 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 28
 gatgagatag ttgcatacg 20

 <210> 29
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 29
 cgtatgcgaa ctatctcatc gacaacggcg aggcttcgac tgc 43

 <210> 30
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 30
 cgaaggtgga tgagttccag 20

 <210> 31
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 31
 ctggaactca tccaccttcg acctctggga agaagtagaa gg 42

 <210> 32
 <211> 21

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 32
 gacaatactc agatatccat c 21

 <210> 33
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 33
 gatggatatc tgagtattgt cgagaaatat actccctcag acg 43

 <210> 34
 <211> 2748
 <212> DNA
 <213> Talaromyces emersonii

 <400> 34
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 tcatagaagc ccttgaaaat accccaagct agcactccaa ccctaactct gttgctctac 120
 tagatcaaga cgagtactct gattgagctg caggcttggga atatatgatt agcagaaaaa 180
 ggggttaaaac ttgtatgaca atcagtttgt cagtactccg tagtgatgcc atgtctatag 240
 agtcgacact aaggcagcat gtgaatgagt cggaaatgac aggaagcaga ttccttaaca 300
 gtcatgttct ccgtgcctgc atccccacgt cacctgcaaa gatgcgacgc tactccacac 360
 cggcgccttg atgtctgctg ttcttggcct agtggagccc catgcgctgc tagctcgtgg 420
 tcttcgaata aatcagaata aaaaacggag taattaattg cgcccgcaac aaactaagca 480
 atgtaactca atgccaagct tccgctgatg ctcttgacat ctccgtagtg gcttctttcg 540
 taatttcaga cgtatatata gtagtaatgc ccagcaggcc gggataatga tggggatttc 600
 tgaactctca gcttccgtac gctgaacagt ttgcttgctg tgtcaaccat ggcgtccctc 660
 gttgctggcg ctctctgcat cctgggcctg acgcctgctg catttgacg agcgcccgtt 720
 gcagcgcgag ccaccgggtc cctggactcc tttctcgaa ccgaaactcc aattgccctc 780
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Ile Ala Gly Asn Lys Asp Leu Glu Gln Thr Ile Gln Gln Tyr Ile Ser
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Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu
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Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly
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